SEQUENCE LISTING

<110> Corrado FOGHER

<120> SYNTHETIC POLYNUCLEOTIDE CODING FOR HUMAN LACTOFERRIN, VECTORS, CELLS AND TRANSGENIC PLANTS CONTAINING IT

<130> 4161-14 / X89727RVP

<140> 09/743,823
<141> 2001-08-22

<150> PCT/IT99/00226
<151> 1999-07-19

<150> IT RM98A000478
<151> 1998-07-17

<160> 26

<170> MS Word

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<222> (1)..(2076)

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gcc aca aaa tgc ttc caa tgg caa agg aat atg aga aaa gtt cgt gga   96
Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Lys Val Arg Gly
             20                  25                  30

cct cct gta tct tgc ata aag aga gat tca ccc atc cag tgt atc cag   144
Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys Ile Gln
         35                  40                  45

gca att gcg gaa aac aga gct gat gct gtg act ctt gat ggt ggt ttc   192
Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly Gly Phe
     50                  55                  60

ata tac gag gca gga ctt gcc cca tac aaa ctg cga cct gta gcg gcg   240
Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val Ala Ala
 65                  70                  75                  80

gaa gtc tac ggg acc gaa aga caa cca cga act cac tat tat gct gtg   288
Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr Ala Val
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                    85                  90                  95

gct gtt gtg aag aag ggc gga tct ttt cag ctg aac gaa ctt caa ggt   336
Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu Gln Gly
            100                 105                 110

ctg aag tca tgc cac aca gga ctt cgc agg acc gct gga tgg aat gtc   384
Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp Asn Val
        115                 120                 125

cct ata ggg aca ctt cgt cca ttc ttg aat tgg acg ggt cca cct gag   432
Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro Pro Glu
    130                 135                 140

ccc att gag gca gct gtg gca aga ttc ttc tca gcc tct tgt gtt cca   480
Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val Pro
145                 150                 155                 160

ggt gca gat aaa gga caa ttc ccc aac ctt tgt cgc ctg tgt gcg ggg   528
Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala Gly
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aca ggg gaa aac aaa tgt gca ttc tca tcc cag gaa ccg tac ttc agc   576
Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe Ser
            180                 185                 190

tac tct ggt gcc ttt aag tgt ctt aga gac ggt gct gga gat gtt gct   624
Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val Ala
        195                 200                 205

ttt att aga gag agc aca gtg ttt gag gat ctt tca gac gag gct gaa   672
Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala Glu
    210                 215                 220

agg gac gag tat gag tta ctc tgc cca gac aac act cgt aag cca gtt   720
Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro Val
225                 230                 235                 240

gac aag ttc aaa gat tgc cat ctt gca cgg gtc cct tct cat gcc gtt   768
Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala Val
                245                 250                 255

gtg gca cga agt gtt aat gga aag gag gat gcc atc tgg aat ctt ctc   816
Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu Leu
            260                 265                 270

cgc caa gca cag gaa aag ttt gga aag gac aag tca ccg aaa ttc cag   864
Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe Gln
        275                 280                 285

ctc ttt ggt tcc cct agt ggg cag aaa gat ctt ctg ttc aag gac tct   912
Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp Ser
    290                 295                 300

gcc att ggg ttt tcg aga gtg cca cct agg ata gat tct ggg ttg tac   960
Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu Tyr
305                 310                 315                 320
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ctt ggc tcc gga tac ttt act gca att cag aac ttg agg aaa agt gag   1008
Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser Glu
                325                 330                 335

gag gaa gtt gct gcc cgg cgt gcg cgg gtc gtt tgg tgt gcg gtg gga   1056
Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val Gly
            340                 345                 350

gag caa gag ttg cgc aag tgt aac cag tgg agt ggt ttg agc gaa gga   1104
Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu Gly
        355                 360                 365

tct gtg acc tgc tca tcg gcc tcc act aca gaa gat tgc atc gcc ctg   1152
Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala Leu
    370                 375                 380

gtg ttg aaa gga gaa gct gat gcc atg agt ttg gat gga gga tat gtt   1200
Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr Val
385                 390                 395                 400

tac act gca ggt aaa tgt ggt ttg gtg cct gtc ctt gca gag aac tac   1248
Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr
                405                 410                 415

aaa tca caa caa agc agt gac cct gat cct aac tgt gtg gat aga cct   1296
Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg Pro
            420                 425                 430

gtg gaa gga tat ctt gct gtg gcg gtg gtt agg aga tca gac act agc   1344
Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr Ser
        435                 440                 445

ctt acc tgg aac tct gtg aaa ggc aag aag tcc tgc cac acc gcc gtg   1392
Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala Val
    450                 455                 460

gac agg act gca ggt tgg aat atc ccc atg gga ttg ctc ttc aac cag   1440
Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn Gln
465                 470                 475                 480

acg ggc tcc tgc aaa ttt gat gaa tat ttc agt caa agc tgt gcc cct   1488
Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala Pro
                485                 490                 495

ggt tct gac cca aga tct aat ctc tgt gct ttg tgt att gga gat gag   1536
Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp Glu
            500                 505                 510

caa ggt gag aat aag tgc gtt ccc aac agc aac gag aga tac tac ggt   1584
Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr Gly
        515                 520                 525

tac act ggg gct ttc cgt tgc ttg gct gag aat gct gga gac gtt gca   1632
Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val Ala
    530                 535                 540
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ttt gtg aaa gat gtc act gtc ttg cag aac act gat gga aat aac aat   1680
Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn Asn
545                 550                 555                 560

gag gca tgg gct aag gat ttg aag ctt gca gac ttt gcg ttg ctg tgc   1728
Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu Cys
                565                 570                 575

ctc gat ggc aaa cgt aag cct gtg act gaa gct aga agc tgc cat ctt   1776
Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His Leu
            580                 585                 590

gcc atg gcc ccg aat cat gct gtg gtg tct cgt atg gat aag gtg gaa   1824
Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val Glu
        595                 600                 605

cgc ttg aaa cag gtg ttg ctc cac caa cag gct aaa ttt ggt aga aat   1872
Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg Asn
    610                 615                 620

gga tct gac tgc ccg gac aag ttt tgc tta ttc cag tct gaa acc aaa   1920
Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr Lys
625                 630                 635                 640

aac ctt ttg ttc aat gac aac act gag tgt ctt gcc aga ctc cat ggc   1968
Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His Gly
                645                 650                 655

aaa aca aca tat gaa aaa tat ttg gga cca cag tat gtc gca ggc att   2016
Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly Ile
            660                 665                 670

act aat ctg aaa aag tgc tca acc tcc cca ctc cta gaa gcc tgt gaa   2064
Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala Cys Glu
        675                 680                 685

ttc cta agg aag taa                                              2079
Phe Leu Arg Lys
    690
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<220>
<223> Description of Artificial Sequence: Synthetic DNA

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<400> 5
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<210> 6
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 6
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<210> 7
<211> 36
<212> DNA
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<220>
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<400> 7
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<210> 8

<211> 250
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<213> Artificial Sequence

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gaagtctacg 250

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<212> DNA
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aagacactta aaggcaccag agtagctgaa gtacggttcc tgggatgaga atgcacattt 180
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<212> DNA
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<223> Description of Artificial Sequence: Synthetic DNA

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acttcgtgcc acaacggcat gagaagggac ccgtgcaaga tggcaatctt tgaacttgtc 240
aactggctta cgagt 255

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<223> Description of Artificial Sequence: Synthetic DNA

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

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ttatccgact cagtc 75

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

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<223> Description of Artificial Sequence: Synthetic DNA

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<212> DNA
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<223> Description of Artificial Sequence: Synthetic DNA

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ttattctcac cttgctcatc tccaatacac aaagcacaga gattagatct tgggtcagaa 180
ccaggggcac agctttgact gaaatattca tcaaatttgc aggagcccgt ctggttgaag 240
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

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tctagcttca gtcacaggct tacgtttgcc atcgaggcac agcaacgcaa agtctgcaag 180
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

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<210> 19
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA

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<223> Description of Artificial Sequence: Synthetic DNA

<400> 20
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<210> 21
<211> 1367
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic DNA

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ttttaaggca attaagcatg tttgataaaa tatatatatt gttataaata cttttcaaaa 180
gtataaagtt gatgatggcg tggtggtaga ttattttagt tctaggttcg aatgcaagtt 240
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<211> 962
<212> DNA
<213> Artificial Sequence

<220>
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ataatatatt tatattttaa tatctattct tatgtatttt ttaaaaatct attatatatt 180
gatcaactaa aatattttta tatctacact tattttgcat ttttatcaat tttcttgcgt 240
tttttggcat atttaataat gactattctt taataatcaa tcattattct tacatggtac 300
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tcaacccatc atgagcccac acatttgttg tttctaaccc aacctcaaac tcgtattctc 780
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ct 962

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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic human lactoferrin

<400> 23
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Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Lys Val Arg Gly
20 25 30

Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys Ile Gln
35 40 45

Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly Gly Phe
50 55 60

Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val Ala Ala
65 70 75 80

Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr Ala Val
85 90 95

Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu Gln Gly
100 105 110

Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp Asn Val
115 120 125

Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro Pro Glu
130 135 140

Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val Pro
145 150 155 160

Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala Gly
165 170 175

Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe Ser
180 185 190

Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val Ala
195 200 205

Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala Glu
210 215 220

Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro Val
225 230 235 240

Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala Val
245 250 255

Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu Leu
260 265 270

Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe Gln
275 280 285

Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp Ser
290 295 300

Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu Tyr
305 310 315 320

Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser Glu
325 330 335

Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val Gly
340 345 350

Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu Gly
355 360 365

Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala Leu
370 375 380

Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr Val
385 390 395 400

Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr
405 410 415

Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg Pro
420 425 430

Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr Ser
435 440 445

Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala Val
450 455 460

Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn Gln
465 470 475 480

Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala Pro
485 490 495

Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp Glu
500 505 510

Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr Gly
515 520 525

Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val Ala
530 535 540

Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn Asn
545 550 555 560

Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu Cys
565 570 575

Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His Leu
580 585 590

Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val Glu
595 600 605

Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg Asn
610 615 620

Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr Lys
625 630 635 640

Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His Gly
645 650 655

Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly Ile
660 665 670

Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala Cys Glu
675 680 685

Phe Leu Arg Lys
690

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<211> 1157

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA gmbpsp

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aaaaacaatt attatatcaa aatggcaaaa catttaatac gtattattta ttaaaaaaat 120
atgtaataat atatttatat tttaatatct attcttatgt atttttttaaa aatctattat 180
atattgatca actaaaatat ttttatatct acacttattt tgcattttta tcaattttct 240
tgcgtttttt ggcatattta atatgactat tctttaataa tcaatcatta ttcttacatg 300
gtacatattg ttggaaccat atgaagtgtt cattgcattt gactatgtgg atagtgtttt 360
gatccatgcc cttcatttgc cgctattaat taatttggta acagattcgt tctaatcagt 420
tacttaatcc ttcctcatca taattaatct ggtagttcga atgccataat attgattagt 480
tttttggacc ataagaaaaa gccaaggaac aaaagaagac aaaacacatg agagtatcct 540
ttgcatagca atgtctaagt tcataaaatt caaacaaaaa cgcaatcaca cacagtggac 600
atcacttatc cactagctga tcaggatcgc cgcgtcaaga aaaaaaaact ggaccccaaa 660
agccatgcac aacaacacgt actcacaaag gcgtcaatcg agcgcccaaa acattcacca 720
actcaaccca tcatgagccc acacatttgt tgtttctaac ccaacctcaa actcgtattc 780
tcttccgcca ctcatttttg tttatttcaa cacccgtcaa actgcatccc accccgtggc 840
caaatgttca tgcatgttaa caagacctat gactataaat atctgcaatc tcggcccaag 900
ttttcatcat caagaaccag ttcaatatcc tagtacgccg tattaaagaa tttaagatat 960
actatgatga gagcgcggtt cccattactg ttgctgggag ttgttttcct agcatcagtt 1020
tctgtctcat ttggcattgc gtattgggaa aagcaaaccc cagtcacaac aagtgcctcc 1080
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tccttaaggt gggatcc 1157

<210> 25
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic DNA PCONGT7Sp6

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<222> (534)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (763)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (787)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (789)
<223> a, t, c, g, other or unknown

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<221> modified_base
<222> (878)
<223> a, t, c, g, other or unknown

<400> 25
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aaaaacaatt attatatcaa aatggcaaaa acatttaata cctattattt aagaaaaaaa 120
tatgtaataa tatatttata ttttaatatc tattcttatg tatttttaa aaatctatta 180
tatattgatc aactaaaata ttttttatatc tacacttatt ttgcattttt atcaattttc 240
ttgcgttttt tggcatattt aataatgact attctttaat aattaatcat tattcttaca 300
tcgtacatat tgttggaacc atatgaagtg tccattgcat tcgactatgt ggatagtgtt 360
ttgatccagg cctccatttg ccgcttatta attaatttgg taacagtccg tactaatcag 420
ttacttatcc ttcctccatc ataattaatc ttggtagtct cgaatgccac aacactgact 480
agtctcttgg atcataagaa aaagccaaga acaaaaggag acaaaacaca atgnagagta 540
tcctttgcat agcaatgtct aagttcataa aattcaaaca aaaacgcaat cacacacagt 600
gggacatcac ttatccacta gctgatcagg atcgccgcgt caagaaaaaa aaaactggga 660
cccaaaagcc atgcacaaca acacgtactc acaaaggtgt caatcgagca gcccaaaaca 720
ttcaccaact caacccatca tgagcccaca catttgttgt ttntaaccca acctcaaact 780
cgtattntnt tccgccacct catttttgtt tattccaaca cccgtcaaac tgcatgccac 840
cccgtggcca aatgtccatg catgttaaca agacctanga ctataaatat ctgcaatctc 900
ggcccaggtt ttcatcatca agaaccagtt caatatccta gtacaccgta ttaaagaatt 960
taagatatac tatgatgaga gcgcggttcc cattactgtt gctggagttg ttttcctggc 1020
atcagtttct gtctcatttg gcattgcgta ttgggaaaag cagaacccca gtcacaacaa 1080
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<210> 26
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic signal peptide

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1 5 10 15

Phe Leu Phe Phe Leu Ser Asp Ser Val
20 25